OIPE

```
RAW SEQUENCE LISTING              DATE: 01/04/2001
PATENT APPLICATION:  US/09/734,002    TIME: 09:37:13

Input Set : A:\seiki sequence listing.txt
Output Set: N:\CRF3\01042001\I734002.raw
                SEQUENCE LISTING
C-->   3 (1) GENERAL INFORMATION:
       5      (i) APPLICANT: Motoharu SEIKI et al.
       7     (ii) TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO
       9    (iii) NUMBER OF SEQUENCES: 14
      11     (iv) CORRESPONDENCE ADDRESS:
      12          (A) ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
      13          (B) STREET: 2033 K Street, N.W., Suite 800
      14          (C) CITY: Washington
      15          (D) STATE: D.C.
      16          (E) COUNTRY: U.S.A.
      17          (F) ZIP: 20006
      19      (v) COMPUTER READABLE FORM:
      20          (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
      21          (B) COMPUTER: IBM Compatible
      22          (C) OPERATING SYSTEM: MS-DOS
      23          (D) SOFTWARE: Wordperfect 5.1
      30     (vi) CURRENT APPLICATION DATA:
C--> 31          (A) APPLICATION NUMBER: US/09/734,002
C--> 32          (B) FILING DATE: 12-Dec-2000
      33          (C) CLASSIFICATION:
      35    (vii) PRIOR APPLICATION DATA:
C--> 36          (A) APPLICATION NUMBER: PCT/JP96/01956
C--> 37          (B) FILING DATE: July 12, 1996
C--> 39   (viii) ATTORNEY/AGENT INFORMATION:
      40          (A) NAME: Lee Cheng
      41          (B) REGISTRATION NUMBER: 40,949
      42          (C) REFERENCE/DOCKET NUMBER:
      44     (ix) TELECOMMUNICATION INFORMATION:
      45          (A) TELEPHONE: 202-721-8200
      46          (B) TELEFAX: 202-721-8250
      47          (C) TELEX:


ERRORED SEQUENCES

     229 (2) INFORMATION FOR SEQ ID NO: 2:
     231      (i) SEQUENCE CHARACTERISTICS:
     232          (A) LENGTH: 607
     233          (B) TYPE: Amino acid
     234          (C) STRANDEDNESS: Single
     235          (D) TOPOLOGY: Linear
     237     (ii) MOLECULE TYPE: Protein
     239     (vi) ORIGINAL SOURCE:
     240          (A) ORGANISM: Human
C--> 242     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
     244 Met Ile Leu Leu Thr Phe Ser Thr Gly Arg Arg Leu Asp Phe Val His
```

Does Not Comply
Corrected Diskette Needed

See p. 2

```
245  1                  5                      10                     15
247 His Ser Gly Val Phe Phe Leu Gln Thr Leu Leu Trp Ile Leu Cys Ala
248                20                     25                     30
250 Thr Val Cys Gly Thr Glu Gln Tyr Phe Asn Val Glu Val Trp Leu Gln
251            35                     40                     45
253 Lys Tyr Gly Tyr Leu Pro Pro Thr Asp Pro Arg Met Ser Val Leu Arg
254         50                     55                     60
256 Ser Ala Glu Thr Met Gln Ser Ala Leu Ala Ala Met Gln Gln Phe Tyr
257     65                     70                     75                 80
259 Gly Ile Asn Met Thr Gly Lys Val Asp Arg Asn Thr Ile Asp Trp Met
260                85                     90                     95
262 Lys Lys Pro Arg Cys Gly Val Pro Asp Gln Thr Arg Gly Ser Ser Lys
263            100                    105                    110
265 Phe His Ile Arg Arg Lys Arg Tyr Ala Leu Thr Gly Gln Lys Trp Gln
266        115                    120                    125
268 His Lys His Ile Thr Tyr Ser Ile Lys Asn Val Thr Pro Lys Val Gly
269     130                    135                    140
271 Asp Pro Glu Thr Arg Lys Ala Ile Arg Arg Ala Phe Asp Val Trp Gln
272 145                    150                    155                    160
274 Asn Val Thr Pro Leu Thr Phe Glu Glu Val Pro Tyr Ser Glu Leu Glu
275                165                    170                    175
277 Asn Gly Lys Arg Asp Val Asp Ile Thr Ile Ile Phe Ala Ser Gly Phe
278            180                    185                    190
280 His Gly Asp Ser Ser Pro Phe Asp Gly Glu Gly Gly Phe Leu Ala His
281     195                    200                    205
283 Ala Tyr Phe Pro Gly Pro Gly Ile Gly Gly Asp Thr His Phe Asp Ser
284         210                    215                    220
286 Asp Glu Pro Trp Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu
287 225                    230                    235                    240
289 Phe Leu Val Ala Val His Glu Leu Gly His Ala Leu Gly Leu Glu His
290                245                    250                    255
292 Ser Asn Asp Pro Thr Ala Ile Met Ala Pro Phe Tyr Gln Tyr Met Glu
293                260                    265                    270
295 Thr Asp Asn Phe Lys Leu Pro Asn Asp Asp Leu Gln Gly Ile Gln Lys
296         275                    280                    285
298 Ile Tyr Gly Pro Pro Asp Lys Ile Pro Pro Pro Thr Arg Pro Leu Pro
299     290                    295                    300
301 Thr Val Pro Pro His Arg Ser Ile Pro Pro Ala Asp Pro Arg Lys Asn
302 305                    310                    315                    320
304 Asp Arg Pro Lys Pro Pro Arg Pro Pro Thr Gly Arg Pro Ser Tyr Pro
305         325                    330                    335
307 Gly Ala Lys Pro Asn Ile Cys Asp Gly Asn Phe Asn Thr Leu Ala Ile
308         340                    345                    350
310 Leu Arg Arg Glu Met Phe Val Phe Lys Asp Gln Trp Phe Trp Arg Val
311     355                    360                    365
313 Arg Asn Asn Arg Val Met Asp Gly Tyr Pro Met Gln Ile Thr Tyr Phe
31  370                    375                    380
316 Trp Arg Gly Leu Pro Pro Ser Ile Asp Ala Val Tyr Glu Asn Ser Asp
317 375                    390                    395                    400
```
E--> 317 375

Invalid amino acid number. Should be 385. (handwritten)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/734,002

DATE: 01/04/2001
TIME: 09:37:14

Input Set : A:\seiki sequence listing.txt
Output Set: N:\CRF3\01042001\I734002.raw

```
319 Gly Asn Phe Val Phe Phe Lys Gly Asn Lys Tyr Trp Val Phe Lys Asp
320              405              410              415
322 Thr Thr Leu Gln Pro Gly Tyr Pro His Asp Leu Ile Thr Leu Gly Ser
323              420              425              430
325 Gly Ile Pro Pro His Gly Ile Asp Ser Ala Ile Trp Trp Glu Asp Val
326          435              440              445
328 Gly Lys Thr Tyr Phe Phe Lys Gly Asp Arg Tyr Trp Arg Tyr Ser Glu
329     450              455              460
331 Glu Met Lys Thr Met Asp Pro Gly Tyr Pro Lys Pro Ile Thr Val Trp
332 465              470              475              480
334 Lys Gly Ile Pro Glu Ser Pro Gln Gly Ala Phe Val His Lys Glu Asn
335              485              490              495
337 Gly Phe Thr Tyr Phe Tyr Lys Gly Lys Glu Tyr Trp Lys Phe Asn Asn
338          500              505              510
340 Gln Ile Leu Lys Val Glu Pro Gly His Pro Arg Ser Ile Leu Lys Asp
341          515              520              525
343 Phe Met Gly Cys Asp Gly Pro Thr Asp Arg Val Lys Glu Gly His Ser
344     530              535              540
346 Pro Pro Asp Asp Val Asp Ile Val Ile Lys Leu Asp Asn Thr Ala Ser
347 545              550              555              560
349 Thr Val Lys Ala Ile Ala Ile Val Ile Pro Cys Ile Leu Ala Leu Cys
350              565              570              575
352 Leu Leu Val Leu Val Tyr Thr Val Phe Gln Phe Lys Arg Lys Gly Thr
353          580              585              590
355 Pro Arg His Ile Leu Tyr Cys Lys Arg Ser Met Gln Glu Trp Val
356          595              600              605
```

VERIFICATION SUMMARY   DATE: 01/04/2001
PATENT APPLICATION: US/09/734,002   TIME: 09:37:15

Input Set : A:\seiki sequence listing.txt
Output Set: N:\CRF3\01042001\I734002.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:39 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:36 M:220 C: Keyword misspelled or invalid format, (A) APPLICATION NUMBER:
L:37 M:220 C: Keyword misspelled or invalid format, (B) FILING DATE:
L:62 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:242 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:317 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:370 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:386 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:401 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:416 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:432 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:446 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:447 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:451 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:462 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:463 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:467 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:478 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:479 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:483 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:494 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:495 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:499 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:510 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:511 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:515 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:531 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:550 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14